WE CLAIM:

A process for identifying a compound which inhibits viral replication that includes contacting
nucleic acids from a virus infected host with an amplification reaction mixture that
contains at least two primers and/or probes that provide detectable signals during a
polymerase chain reaction, wherein

the first primer and/or probe provides a detectable signal on the occurrence of the transcription of viral nucleic acids; and

the second primer and/or probe provides a second detectable signal on the occurrence of the transcription of host nucleic acids.

- 2. The process of claim 1, wherein the host nucleic acid is nuclear nucleic acid.
- 3. The process of claim 1, wherein the host nucleic acid is mitochondrial nucleic acid.
- 4. The process of claim 3, wherein the mitochondrial nucleic acid is mitochondrial DNA.
- 5. The process of claim 3, wherein the mitochondrial nucleic acid is mitochondrial RNA.
- 6. The process of claim 1, wherein the viral nucleic acid is a non-coding sequence.
- 7. The process of claim 6, wherein the non-coding sequence is a 5'-non-coding sequence.





- 8. The process of claim 6, wherein the non-coding sequence is a 3'-non-coding sequence.
- 9. The process of claim 6, wherein the non-coding sequence is an intron.
- 10. The process of claim 6, wherein the non-coding sequence is from β -actin.
- 11. The process of claim 6, wherein the non-coding sequence is from GAPDH.
- 12. The process of claim 1, wherein the viral nucleic acid is a coding sequence.
- 13. The process of claim 12, wherein the coding sequence is from HIV.
- 14. The process of claim 12, wherein the coding sequence is from HBV.
- 15. The process of claim 12, wherein the coding sequence is from HCV.
- 16. The process of claim 12, wherein the coding sequence is from BVDV.
- 17. The process of claim 12, wherein the coding sequence is from West Nile Virus.
- 18. The process of claim 12, wherein the coding sequence is from herpes.





- 19. The process of claim 12, wherein the coding sequence is from influenza.
- 20. The process of claim 12, wherein the coding sequence is from RSV.
- 21. The process of claim 12, wherein the coding sequence is from EBV.
- 22. The process of claim 12, wherein the coding sequence is from CMV.
- 23. A process for assessing the toxicity of a compound that includes contacting nucleic acids from a host with an amplification reaction mixture that contains at least two primers and/or probes that provide detectable signals during a polymerase chain reaction, wherein

the first primer and/or probe provides a detectable signal on the occurrence on the transcription of host mitochondrial nucleic acids; and

the second primer and/or probe provides a second detectable signal on the occurrence on the transcription of host nuclear nucleic acid.

- 24. The process of claim 23, wherein the host mitochondrial nucleic acid is mitochondrial DNA.
- 25. The process of claim 23, wherein the host mitochondrial nucleic acid is mitochondrial RNA.
- 26. The process of claim 23, wherein the host mitochondrial nucleic acid is a non-coding sequence.





- 27. The process of claim 26, wherein the non-coding sequence is a 5'-non-coding sequence.
- 28. The process of claim 26, wherein the non-coding sequence is a 3'-non-coding sequence.
- 29. The process of claim 26, wherein the non-coding sequence is an intron.
- 30. The process of claim 26, wherein the non-coding sequence is from β -actin.
- 31. The process of claim 26, wherein the non-coding sequence is from GAPDH.
- 32. The process of claim 23, wherein the host mitochondrial nucleic acid is a coding sequence.